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Application Serial Number: _10/612,466_

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Revised 04/24/2003

OIPE

RAW SEQUENCE LISTING   DATE: 08/11/2003
PATENT APPLICATION: US/10/612,466   TIME: 13:38:59

Input Set : A:\1625seq.001
Output Set: N:\CRF4\08112003\J612466.raw

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 3 <110> APPLICANT: Madison, Edwin
 4        Ong, Edgar
 5        Yeh, Juinn-Chern
 7 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING SERINE PROTEASE 16, THE
 8        ENCODED PROTEINS AND METHODS BASED THEREON
10 <130> FILE REFERENCE: 24745-1625
12 <140> CURRENT APPLICATION NUMBER: US/10/612,466
13 <141> CURRENT FILING DATE: 2003-07-01
15 <150> PRIOR APPLICATION NUMBER: 60/394,347
16 <151> PRIOR FILING DATE: 02-JUL-02  2002-07-02
18 <160> NUMBER OF SEQ ID NOS: 22
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3147
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo Sapien
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (23)...(2589)
30 <223> OTHER INFORMATION: Nucleotide sequence encoding MTSP1
32 <300> PUBLICATION INFORMATION:
33 <308> DATABASE ACCESSION NO: GenBank #AR081724
34 <309> DATABASE ENTRY DATE: 2000-08-31
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41 ggg ggc ccg aag gac ttc ggc gcg gga ctc aag tac aac tcc cgg cac  100
42 Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His
43                 15                  20                  25
45 gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac  148
46 Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn
47             30                  35                  40
49 aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg  196
50 Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu
51             45                  50                  55
53 gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc  244
54 Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe
55         60                  65                  70
57 ctg gtg tgg cat ttg cag tac cgg gac gtg cgt gtc cag aag gtc ttc  292
58 Leu Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe
59 75                  80                  85                  90
61 aat ggc tac atg agg atc aca aat gag aat ttt gtg gat gcc tac gag  340
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Input Set : A:\1625seq.001
Output Set: N:\CRF4\08112003\J612466.raw

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 66 Asn Ser Asn Ser Thr Glu Phe Val Ser Leu Ala Ser Lys Val Lys Asp
 67             110             115             120
 69 gcg ctg aag ctg ctg tac agc gga gtc cca ttc ctg ggc ccc tac cac   436
 70 Ala Leu Lys Leu Leu Tyr Ser Gly Val Pro Phe Leu Gly Pro Tyr His
 71         125             130             135
 73 aag gag tcg gct gtg acg gcc ttc agc gag ggc agc gtc atc gcc tac   484
 74 Lys Glu Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr
 75         140             145             150
 77 tac tgg tct gag ttc agc atc ccg cag cac ctg gtg gag gag gcc gag   532
 78 Tyr Trp Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu
 79 155             160             165             170
 81 cgc gtc atg gcc gag gag cgc gta gtc atg ctg ccc ccg cgg gcg cgc   580
 82 Arg Val Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg
 83             175             180             185
 85 tcc ctg aag tcc ttt gtg gtc acc tca gtg gtg gct ttc ccc acg gac   628
 86 Ser Leu Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp
 87             190             195             200
 89 tcc aaa aca gta cag agg acc cag gac aac agc tgc agc ttt ggc ctg   676
 90 Ser Lys Thr Val Gln Arg Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu
 91         205             210             215
 93 cac gcc cgc ggt gtg gag ctg atg cgc ttc acc acg ccc ggc ttc cct   724
 94 His Ala Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro
 95     220             225             230
 97 gac agc ccc tac ccc gct cat gcc cgc tgc cag tgg gcc ctg cgg ggg   772
 98 Asp Ser Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly
 99 235             240             245             250
101 gac gcc gac tca gtg ctg agc ctc acc ttc cgc agc ttt gac ctt gcg   820
102 Asp Ala Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala
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109 agc ccc atg gag ccc cac gcc ctg gtg cag ttg tgt ggc acc tac cct   916
110 Ser Pro Met Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro
111         285             290             295
113 ccc tcc tac aac ctg acc ttc cac tcc tcc cag aac gtc ctg ctc atc   964
114 Pro Ser Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile
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117 aca ctg ata acc aac act gag cgg cgg cat ccc ggc ttt gag gcc acc  1012
118 Thr Leu Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr
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121 ttc ttc cag ctg cct agg atg agc agc tgt gga ggc cgc tta cgt aaa  1060
122 Phe Phe Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg Lys
123             335             340             345
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133 aag gtg agc ttc aaa ttc ttc tac ctg ctg gag ccc ggc gtg cct gcg   1204
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135               380               385               390
137 ggc acc tgc ccc aag gac tac gtg gag atc aat ggg gag aaa tac tgc   1252
138 Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys
139 395               400               405               410
141 gga gag agg tcc cag ttc gtc gtc acc agc aac agc aac aag atc aca   1300
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143               415               420               425
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154 Cys Arg Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp
155       460               465               470
157 gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc   1492
158 Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala
159 475               480               485               490
161 ggc cac cag ttc acg tgc aag aac aag ttc tgc aag ccc ctc ttc tgg   1540
162 Gly His Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp
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167               510               515               520
169 tgc agt tgt ccg gcc cag acc ttc agg tgt tcc aat ggg aag tgc ctc   1636
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171               525               530               535
173 tcg aaa agc cag cag tgc aat ggg aag gac gac tgt ggg gac ggg tcc   1684
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178 Asp Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His
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182 Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu
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185 tgt gac ggg aag gag gac tgt agc gac ggc tca gat gag aag gac tgc   1828
186 Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys
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197 ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg   1972
198 Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp
199 635             640             645             650
201 ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac   2020
202 Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr
203             655             660             665
205 tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc   2068
206 Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser
207             670             675             680
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211             685             690             695
213 tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gcg ctg   2164
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217 ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc   2212
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221 tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg   2260
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223             735             740             745
225 gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc   2308
226 Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile
227             750             755             760
229 ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac   2356
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247             830             835   .         840
249 cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta ggggccgggg 2599
250 Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val
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255 ctccagggct ccaaatctgc ctagaaaacc tctcgcttcc tcagcctcca aagtggagct 2779
256 gggaggtaga aggggaggac actggtggtt ctactgaccc aactgggggc aaaggtttga 2839
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259 ggctgccgga tctgggctgt ggggcccttg ggccacgctc ttgaggaagc ccaggctcgg 3019
260 aggaccctgg aaaacagacg ggtctgagac tgaaattgtt ttaccagctc ccagggtgga 3079
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274 Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
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279 65                  70                  75                  80
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289 145                 150                 155                 160
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295              195                 200                 205
296 Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
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      Ala Ser Cys Trp Val Leu Gly Trp Lys Glu Pro Gln Asp Arg Val Pro
              50                  55                  60
      Val Ala Ala Ala Val Ser Ile Leu Thr Gln Arg Ile Cys Asp Cys Leu
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what response is the valid one?
If it is "Artificial Sequence" include <<220>-<<223>> section and explanation of source material on <<223> line

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      Phe Phe Pro Leu Gln
                      35
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same error